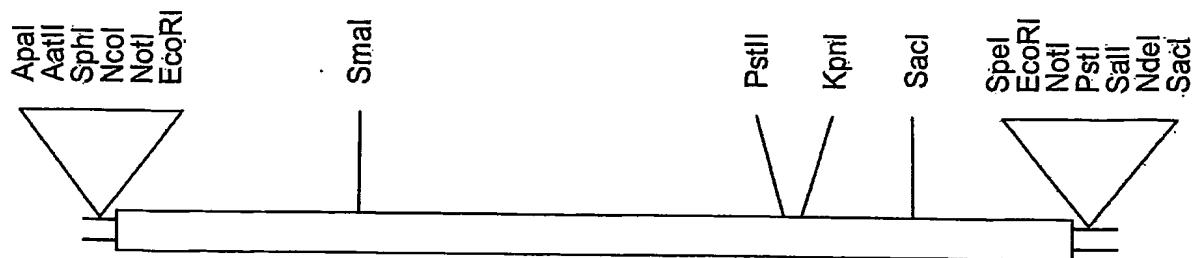


1/40

**TrCHSa3****FIGURE 1**

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1 **GAATTCACTA** GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGAAC
51 **AAAAACA**ACT ACCCATATTA TATATATATA TATATAGTCT ATAATTGAAA
101 **GAAACTG**CTA AAGATATTAT TAAGATATGG TGAGTGTAGC TGAAATTGCG
151 **AAGGCTC**AGA GGGCTGAAGG CCCTGCAACC ATTTGGCCA TTGGCACTGC
201 **AAATCC**ACCA AACCGTGTG AGCAGAGCAC ATATCCTGAT TTCTACTTCA
251 **AAATTAC**AAA CAGTGAGCAC AAGACTGAGC TCAAAGAGAA GTTCCAACGC
301 **ATGTGTG**ACA AATCCATGAT CAAGAGCAGA TACATGTATC TAACAGAAGA
351 **GATTTG**AAA GAAAATCCTA GTCTTGTGA ATACATGGCA CCTTCATTGG
401 **ATGCTAGG**CA AGACATGGTG GTGGTTGAGG TACCTAGACT TGGGAAGGAG
451 **GCTGCAG**TCA AGGCCATTAA AGAATGGGAGT CAACCAAAGT CAAAGATTAC
501 **TCACTTA**ATC TTTGCACCA CAAGTGGTGT TGACATGCCT GGTGCTGATT
551 **ACCAACT**CAC AAAACTCTTA GGTCTTCGCC CATATGTGAA AAGGTATATG
601 **ATGTACCA**AC AAGGTTGTTT TGCAGGAGGC ACGGTGCTTC GTTGGCAAA
651 **AGATTG**GCC GAGAACACA AAGGTGCTCG TGTGCTAGTT GTTGTCTG
701 **AAGTCACC**GC AGTCACATT CGCGGCCCA GTGATACTCA CTTGGACAGT
751 **CTTGTG**GAC AAGCATTGTT TGGAGATGGA GCCGCTGCAC TAATTGTTGG
801 **TTCTG**ATCCA GTGCCTGAAA TTGAGAAACC AATATTGAG ATGGTTGGA
851 **CTGCACAA**AC AATTGCTCCA GACAGTGAAG GTGCCATTGA TGGTCATCTT
901 **CGTGAAG**CTG GGCTAACATT TCATCTTCTT AAAGATGTT CTGGGATTGT
951 **ATCAAAG**AC ATTAATAAAG CATTGGTTGA GGCTTCCAA CCATTAGGAA
1001 **TTTCTG**ACTA CAACTCAATC TTTGGATTG CACACCCGGG TGGACCTGCA
1051 **ATTCTTG**ATC AAGTAGAACAA AAAGCTAGCC TTGAAGCCCG AAAAGATGAG
1101 **GGCCAC**GAGG GAAGTTCTAA GTGAATATGG AAACATGTCA AGCGCATGTG
1151 **TATTG**TTCAT CTTAGATGAG ATGCGGAAGA AATCGGCTCA AAATGGACTT
1201 **AAGACA**ACTG GAGAAGGACT TGATTGGGT GTGTTGTTCG GCTTCGGACC
1251 **AGGACTT**ACC ATTGAAACCG TTGTTCTCG TAGCGTGGCT ATATAAGATG
1301 **TGTG**ATTGTT TTTATTTAA TGTATTACTT TTAATCTTGC TGCCTTGAAT
1351 **TTCG**ATTTAA GAATAAATAA ATATATCTT TGATAAAAAA AAAAAAAA
1401 **AAAAAAAA**AAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CGAATTG

FIGURE 2

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1 MVSVAEIRKA QRAEGPATIL AIGTANPPNR VEQSTYPDFY FKITNSEHKT
51 ELKEKFQRCMC DKSMIKSRYM YLTEEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA VKAIKEWGQP KSKITHLIFC TTSGVDMMPGA DYQLTKLLGL
151 RPYVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEVTAVTFRG
201 PSDTHLDSLV GQALFGDGAA ALIVGSDPVP EIEKPIFEMV WTAQTIAPDS
251 EGAIDGHLRE AGLTFHLLKD VPGIVSKNIN KALVEAFQPL GISDYNNSIFW
301 IAHPGGPAIL DQVEQKLALK PEKMRATREV LSEYGNMSSA CVLFILDEMR
351 KKSAQNGLKT TGEGLDWGVL FGFGPGLTIE TVVLRSAI

FIGURE 3

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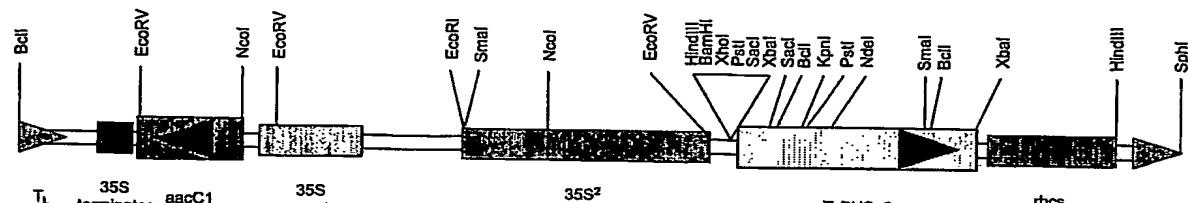
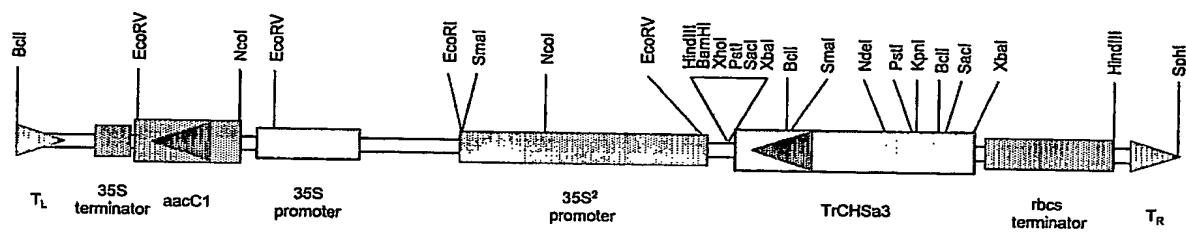
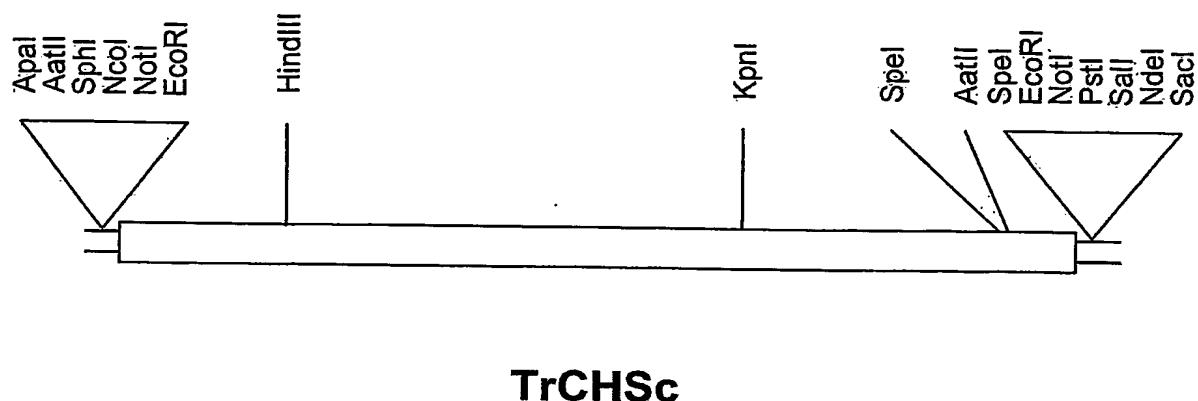
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FIGURE 4

5/40**FIGURE 5**

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1 GAATTCGATT AAGCAGTGGT ACAACGCAG AGTACGCGGG GATTCAATCT
 51 GTTGTGCATA AAATTCACTC ATTGCATAGA AAACCATACA CATTGATCT
 101 TGCAAAGAAG AAATATGGGA GACGAAGGTA TAGTGAGAGG TGTACAAAG
 151 CAGACAACCC CTGGGAAGGC TACTATATTG GCTCTGGCA AGGCATTCCC
 201 TCACCAACTT GTGATGCAAG AGTGTGTTAGT TGATGGTTAT TTTAGGGACA
 251 CTAATTGTGA CAATCCTGAA CTTAAGCAGA AACTTGCTAG ACTTTGTAAG
 301 ACAACCACGG TAAAAACAAG GTATGTTGTT ATGAATGAGG AGATACTAAA
 351 GAAATATCCA GAACTGTTG TCGAAGGCGC CTCAACTGTA AAACAACGTT
 401 TAGAGATATG TAATGAGGCA GTAACACAAA TGGCAATTGA AGCTTCCCAA
 451 GTTGCCTAA AGAATTGGGG TAGATCCTTA TCGGACATAA CTCATGTGGT
 501 TTATGTTCA TCTAGTGAAG CTAGATTACC CGGTGGTGAC CTATACTTGT
 551 CAAAAGGACT AGGACTAAAC CCTAAAATTC AAAGAACCAT GCTCTATTTC
 601 TCTGGATGCT CGGGAGGCCT AGCCGGCCTT CGCGTTGCGA AAGACGTAGC
 651 TGAGAACAAAC CCTGGAAGTA GAGTTTGCT TGCTACTTCG GAAACTACAA
 701 TTATTGGATT CAAGCCACCA AGTGTGATA GACCTTATGA TCTTGTGGT
 751 GTGGCACTCT TTGGAGATGG TGCTGGTGCA ATGATAATTG GCTCAGACCC
 801 GGTATTTGAA ACTGAGACAC CATTGTTGA GCTGCATACT TCAGCTCAGG
 851 AGTTTATACC AGACACCGAG AAGAAAATTG ATGGGCGGCT GACGGAGGAG
 901 GGCATAAGTT TCACACTAGC AAGGGAACCTT CCGCAGATAA TCGAAGACAA
 951 TGTTGAGGGA TTCTGTAATA AACTAATTGA TGTTGTGGG TTGGAGAATA
 1001 AGGAGTACAA TAAGTTGTTT TGGGCTGTGC ATCCAGGTGG GCCTGCGATA
 1051 TTGAATCGCG TGGAGAAGCG GCTTGAGTTG TCGCCGCAGA AGCTGAATGC
 1101 TAGTAGAAAA GCTCTAATGG ATTATGGAAA TGCTAGCAGC AATACTATTG
 1151 TTTATGTGCT GGAATATATG CTAGAAGAGG AAAAGAAGAT TAAAAAGGCG
 1201 GGTGGAGGAG ATTCTGAATG GGGATTGATA CTTGCTTTG GACCTGGAAT
 1251 TACTTTGAG GGGATTCTAG CAAGGAACTT GTGTGCATGA AGTCTTATAC
 1301 AATTGTGATG CATGACTTAT ACTCTTATTT CTACTAATTA TTATATTAAG
 1351 CAAATTCAAGA ACTTTAAGT AATGATTTAA TGAAGAATAC TTATAGTATA
 1401 TTGACTTTAT TCACTTCAA AGCAAGTTA TGATCCTAAG ACATGGTAGA
 1451 ACTTGAGCAT GTGGAATAGT TGTAACAAAA ACTCTAAGCA AATAGAGACT
 1501 TTATGTAGTA TAAAGCATTG CCAGACATGA TAAATAATGG TACCTCAGAA
 1551 CATAAAATAT ATTTAGCTAT CTTTCATCCC CAACTTTACA CATCCACCAA
 1601 GGTACAGAAT AAGCATATGT CAACACAAAA TGTACTCTAA GTCTAACATG
 1651 AGTAACCAAA CATGATGCCT GATTAAGTTA AAAGAAAAGA AAATCTGAGG
 1701 GCATAGATCT TCAATCACAC CACTCCAGAG GGAAGGCGTA GAACAAGCTG

FIGURE 6

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1751 TCCGCCGAAA ACACGTCAAT TCAATAAATA TCATTAGGAC AACAGTCAG
1801 AGTCATGCGG GAAATGTCTT AAGTCACTGT ACTAAAAATA TAGGATTATA
1851 TTATGAACTA TACTAACCTT TTCACATAAT AGTAACAGAA ATCAGCTAAG
1901 ATGAATGTCT GGACAATTTC TGAGATAAGA ACCATGACGG CCATAAGCCA
1951 TACCCCAAGG CAACCAATAA ATGTCCACGG GTATCTAACCA CCTGTTGCAA
2001 GAAATAGTAA GTTATTAGGA GATGTGCGGT TACGAAATTC AAGCTACACA
2051 ACAAAAGGAG GCCAGAACAA CAGCAATCTT GTAACCAGAT GACAACAATA
2101 AAATGTAAAC TTAAAGAGAC CGAACACACA AACATTGCAA CTCAGATGGA
2151 ATTGCTGCCA TGTAACTAGT AGGAGATTG GGACGTCAAA TCAGTATATT
2201 ATGCAAATAC AAGGTATGAC CGCCTTGTCT ATTGTAGCAT ACAACAAACG
2251 TACAGTGGGT TTGTCCCTCT CAAAATGGCA GGATCTTAC AGCACAATAT
2301 TTGGTTTTGT CATACTTATA CCATAAAAAA AAAAAAAA AAAAAAAA
2351 AAAGTACTCT GCGTTGTTAC CACTGCTAA TCACTAGTGA ATTG

FIGURE 6 (cont.)

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1 MGDEGIVRGV TKQTPGKAT ILALGKAFPH QLVMQECLVD GYFRDTNCDN
51 PELKQKLARL CKTTTVKTRY VVMNEEILKK YPELVVEGAS TVKQRLEICN
101 EAVTQMAIEA SQVCLKNWGR SLSDITHVVY VSSSEARLPG GDLYLSKGLG
151 LNPKIQRTML YFSGCSGGVA GLRVAKDVAE NNPGSRVLLA TSETTIIGFK
201 PPSVDRPYDL VGVALFGDGA GAMIIGSDPV FETETPLFEL HTSAQEFIPD
251 TEKKIDGRLT EEGISFTLAR ELPQIIEDNV EGFCNKLIDV VGLENKEYNK
301 LFWAVHPGGP AILNRVEKRL ELSPQKLNAS RKALMDYGNSSNTIVYVLE
351 YMЛЕЕККИК KAGGGDSEWG LILAFGPGIT FEGILARNLC A

FIGURE 7

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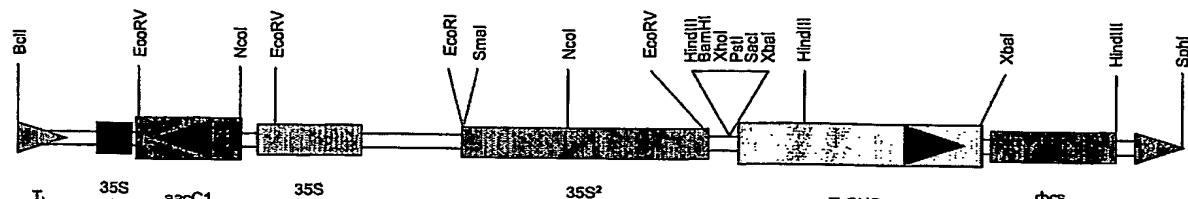
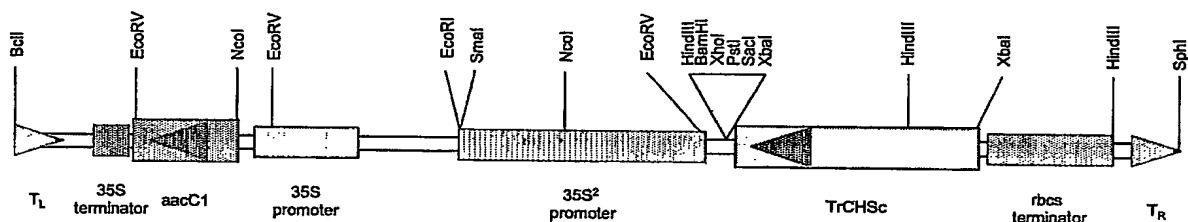
pPZP221:35S²TrCHSc sensepPZP221:35S²TrCHSc anti

FIGURE 8

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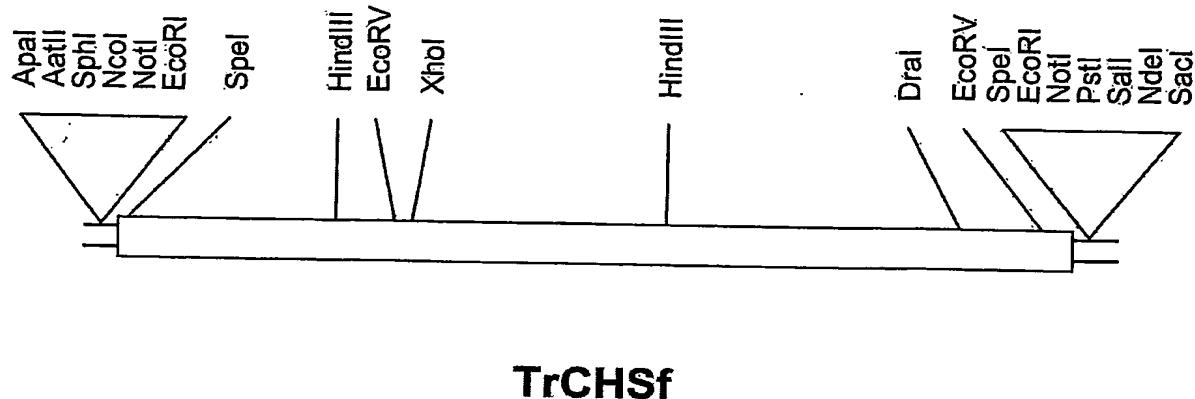


FIGURE 9

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1 GAATTCGATT AAGCAGTGGT AACAAACGAG AGTACGCGGG ACTAAGCCTT
 51 GATTCAATTGT TTGTTTCCAT AACACAAGAA CTAGTGTTCG CTTGAATCTT
 101 AAGAAAAAAAT GCCTCAAGGT GATTGAATG GAAGTTCCCTC GGTGAATGGA
 151 GCACGTGCTA GACGTGCTCC TACTCAGGGA AAGGCAACGA TACTTGCATT
 201 AGGAAAGGCT TTCCCCGCC AGGTCCCTCC TCAAGAGTGC TTGGTGGAAAG
 251 GATTCAATTG CGACACTAAG TGTGACGATA CTTATATTAA GGAGAAATTG
 301 GAGCGTCCTT GCAAAAACAC AACTGTGAAA ACAAGATACA CAGTAATGTC
 351 AAAGGAGATC TTAGACAACAT ATCCAGAGCT AGCCATAGAT GGAACACCAA
 401 CAATAAGGCA AAAAGCTTGAA ATAGCAAATC CAGCAGTAGT TGAAATGGCA
 451 ACAAGAGCAA GCAAAGATTG CATCAAAGAA TGGGGAAAGGT CACCTCAAGA
 501 TATCACACAC ATAGTCTATG TTTCCCTCGAG CGAAATTCTGT CTACCCGGTG
 551 GTGACCTTTA TCTTGCAAAT GAACTCGGCT TAAACAGCGA TGTTAATCGC
 601 GTAATGCTCT ATTTCCCTCGG TTGCTACGGC GGTGTCACTG GCTTACGTGT
 651 CGCCAAAGAC ATCGCCGAAA ATAACCCCTGG TAGTAGGGTG TTACTCACAA
 701 CATCCGAGAC CACTATTCTC GGTTTCGAC CACCGAGTAA AGCTAGACCT
 751 TATGACCTCG TTGGCGCTGC ACTTTTCGGT GATGGCGCCG CTGCTGCAAT
 801 AATTGGAACA GACCCTATAT TGAATCAAGA ATCACCTTTC ATGGAATTGA
 851 ACCATGCGAT CCAAAAATTC TTGCCTGATA CACAAAATGT GATTGATGGT
 901 AGAATCACTG AAGAGGGTAT TAATTTAAG CTTGGAAGAG ACCTTCCTCA
 951 AAAAATTGAA GACAATATTG AAGAATTTCG CAAGAAAATT ATGGCTAAAA
 1001 GTGATGTTAA GGAATTAAAT GACTTATTTT GGGCTGTTCA TCCTGGTGGG
 1051 CCAGCTATAC TCAATAAGCT AGAAAATATA CTCAAATTGA AAAGTGATAA
 1101 ATTGGATTGT AGTAGGAAGG CATTATGGA TTATGGAAAT GTTAGTAGCA
 1151 ATACTATATT CTATGTGATG GAGTATATGA GAGATTATTT GAAGGAAGAT
 1201 GGAAGTGAAG AATGGGGATT AGGATTGGCT TTTGGACCAG GGATTACTTT
 1251 TGAAGGGGTT CTCCTCCGTA GCCTTAATC TTGAAATAAT AATTCAATATG
 1301 AAATTACTTG TCTTAAGATT GTGATAGGAA GATGAATATG TATTGGATTA
 1351 ATATTGATAT GGTGTTATT TAAAGTTGATT TTAAAAAAAG TTTATTAATA
 1401 AAGTATGATG TAACAATTGT TGTTGAATG TTAAAAGGGA AGTATACTAT
 1451 TTTAAGTTCT TGACCATACT GATTTTTCT TTACACATTT TCATATCTAA
 1501 AATTGTTCTA TGATATCTTC ATTGTTGATA CTGTAATAAT ATAATATCTA
 1551 ATTTGGCTGG CAAAATGAAA GATTTTCAC CGAAAAAAA AAAAAAAA
 1601 AAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CACTAGTGAA
 1651 TTC

FIGURE 10

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1 MPQGDLNGSS SVNGARARRA PTQGKATILA LGKAFPAQVL PQECLVEGFI
51 RDTKCDDTYI KEKLERLCKN TTVKTRYTVM SKEILDNYPE LAIDGPTIR
101 QKLEIANPAV VEMATRASKD CIKEWGRSPQ DITHIVYVSS SEIRLPGGDL
151 YLANELGLNS DVNRVMLYFL GCYGGVTGLR VAKDIAENNP GSRVLLTTSE
201 TTILGFRPPS KARPYDLVGA ALFGDGAAAA IIGTDPILNQ ESPFMELNHA
251 VQKFLPDTQN VIDGRITEEG INFKLGRLDP QKIEDNIEEF CKKIMAKSDV
301 KEFNDLFWAV HPGGPAILNK LENILKLKSD KLDCSRKALM DYGNVSSNTI
351 FYVMEYMRDY LKEDGSEEWG LGLAFGPGIT FEGVLLRSL

FIGURE 11

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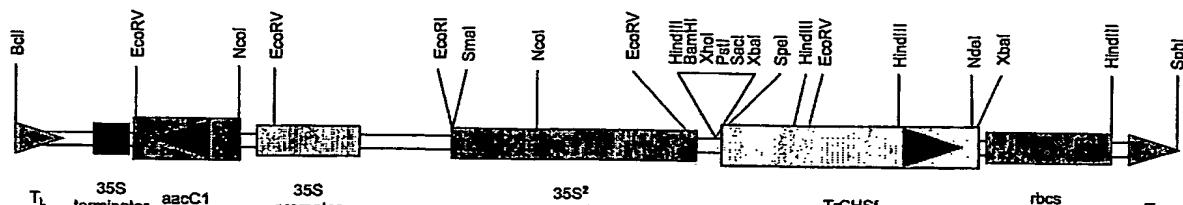
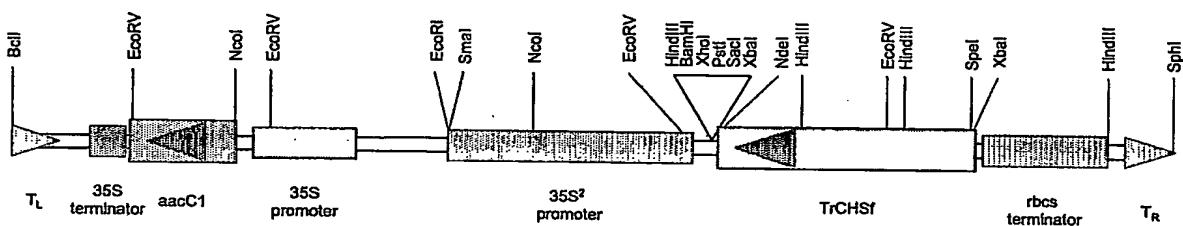
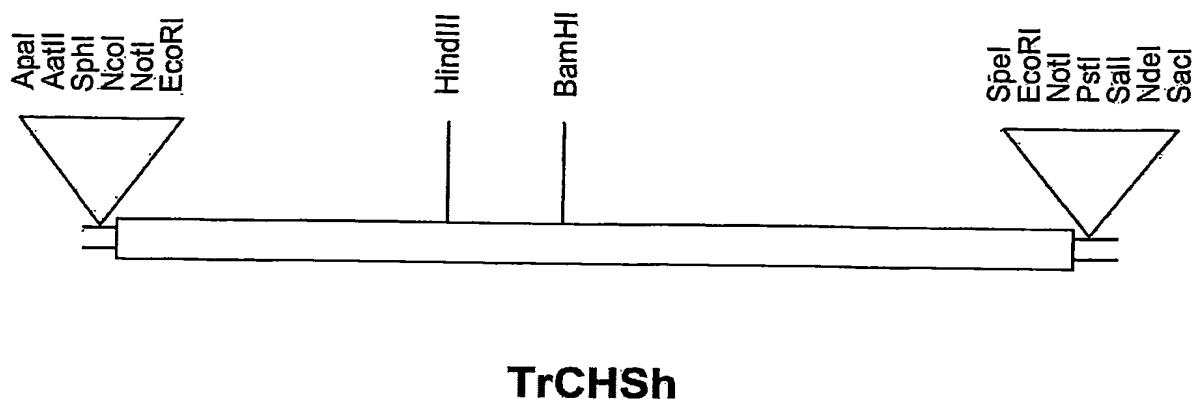
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FIGURE 12

14/40**FIGURE 13**

15/40

1 GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGAA
 51 TCCACCAAAT CAACACCATT AATAACCTTC CAAATTCTCG TTACCTCACC
 101 AAATCTCATT TTTCATTATA TATCTTGGGT ACATCTTTG TTACCTCCAA
 151 CAAAAAAATG GTGACCGTAG AAGAGATTAG TAACGCCAA CGTTCAAATG
 201 GCCCTGCCAC TATCTTAGCT TTTGGCACAG CCACTCCCTC TAACTGTGTC
 251 ACTCAAGCTG ATTATCCTGA TTACTACTTT CGTATCACCA ACAGCGAACAA
 301 TATGACTGAT CTTAAGGAAA AATTCAAGCG GATGTGTGAT AGATCAATGA
 351 TAAAGAAACG TTACATGCAC CTAACAGAAAG ACTTTCTGAA GGAGAATCCA
 401 AATATGTGTG AATACATGGC ACCATCACTA GATGTAAGAC GAGACATAGT
 451 GGTTGTTGAA GTACCAAAGC TAGGTAAAGA AGCAGCAAAA AAAGCCATAT
 501 GTGAATGGGG ACAACCAAAA TCCAAAATCA CACATCTTGT TTTCTGCACC
 551 ACTTCCGGTG TTGACATGCC GGGAGCCGAT TACCAACTCA CCAAACCTTT
 601 AGGCTTAAAAA CCTTCTGTCA AGCGTCTCAT GATGTATCAA CAAGGTTGTT
 651 TCGCTGGCGG CACAGTTCTC CGCTTAGCAA AAGACTTGT TGAGAATAAC
 701 AAAAATGCAA GAGTTCTTGT TGTTGTTCT GAAATTACTG CGGTTACTTT
 751 TCGTGGACCA TCGGATACTC ATCTTGATTC GCTCGTGGGA CAGGCGCTTT
 801 TTGGTGATGG AGCCGCAGCA ATGATTATTG GTGCGGATCC TGATTTAAC
 851 GTGGAGCGTC CGATTTTCA GATTGTTCG GCTGCTCAGA CTATTCTCC
 901 TGATTCTGAT GGCAGCAATTG ATGGACATCT TCGTGAAGTG GGGCTCACTT
 951 TTCATTTATT GAAAGATGTT CCGGGGATTA TTTCAAAGAA CATTGAAAAAA
 1001 AGTTTAGTTG AAGCTTTGC GCCTATTGGG ATTAATGATT GGAACTCAAT
 1051 ATTTTGGGTT GCACATCCAG GTGGACCGGC TATTTAGAC CAGGTTGAAG
 1101 AGAAAATCCA TCTTAAAGAG GAGAAAATCC GGTCCACCCG GCATGTGCTT
 1151 AGTGAATATG GAAATATGTC AAGTGCATGT GTTTTATTAA TTTTGGATGA
 1201 AATGAGAAAG AGGTCTAAAG AGGAAGGGAT GATTACAAT GGTGAAGGGT
 1251 TGGAATGGGG TGTGTTGTTT GGGTTGGAC CGGGTTAAC TGTTGAAACC
 1301 GTTGTGCTTC ATAGTGTCC GGTTCAAGGT TGAATTATT ATACATAGAT
 1351 TGGAAAATAA AATTTGCCTG CCGAGAGATG TGAACTAACT TTGTAGGCAA
 1401 GCTCAAATTA AAGTTTGAGA TAATATTGTG CTTTAGTTAT TATGGTATGT
 1451 AATGTAATGT TTTTACTTTT TTGAAATTC ATGTAATTG ATATGTAAAG
 1501 TAATATGTTT GGGTTGGAAT ATAATTATTT GTTAACTAAA AAAAAAAA
 1551 AAAAAAAA AAAAAGTACT CTGCGTTGTT ACCACTGCTT AATCGAATTC

FIGURE 14

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1 MVTVEEIRNA QRSNGPATIL AFGTATPSNC VTQADYPDYY FRITNSEHMT
51 DLKEKFKRCM DRSMIKKRYM HLTEDFLKEN PNMCEYMAPS LDVRRDIWVV
101 EVPKLGKEAA KKAICEWGQP KSKITHLVFC TTSGVDMMPGA DYQLTKLLGL
151 KPSVKRLMMY QQGCFAGGTV LRLAKDLVEN NKNARVLVVC SEITAVTFRG
201 PSDTHLDSILV GQALFGDGAA AMIIGADPDL TVERPIFEIV SAAQTAILPDS
251 DGAIDGHLRE VGLTFHLLKD VPGIISKNIE KSLVEAFAPI GINDWNSIFW
301 VAHPGGPAIL DQVEEKLHLK EEKLRSTRHV LSEYGNMSSA CVLFILDEMR
351 KRSKEEGMIT TGEGLEWGVL FGFGPGLTVE TVVLHSVPVQ G

FIGURE 15

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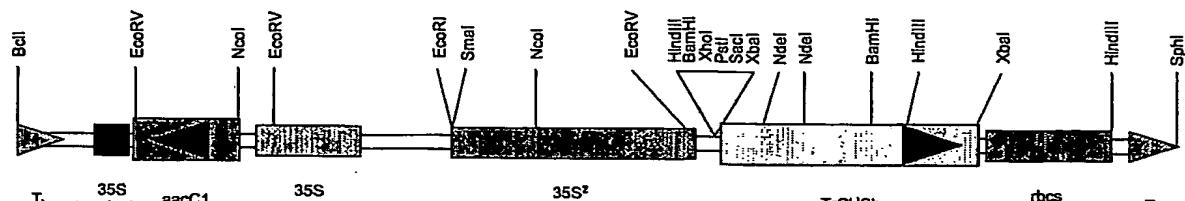
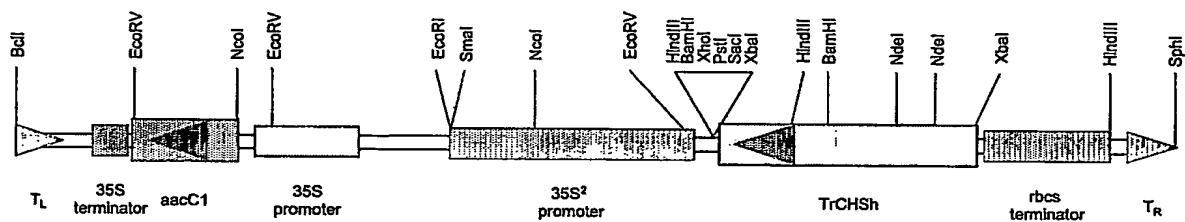
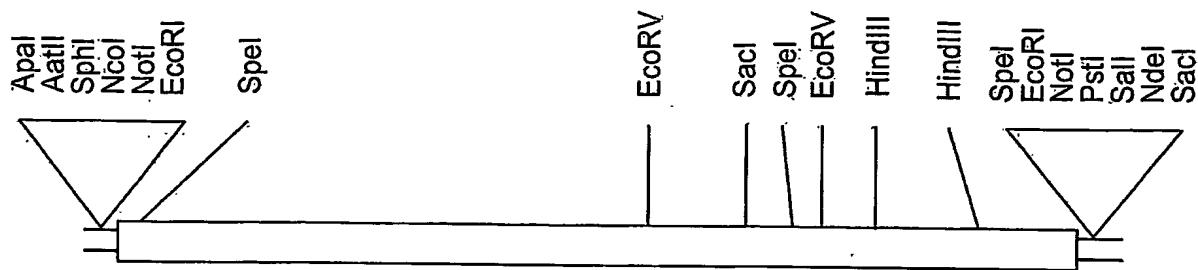
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FIGURE 16

18/40**TrBANa****FIGURE 17**

19/40

1 GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG ATAAAAACTG
51 CACTAGTGTG TATAAGTTTC TTGGTAAAAA AAGAGTTGT AAATTAACAT
101 CATGGCTAGT ATCAAACAAA TTGGAAACAA GAAAGCATGT GTGATTGGTG
151 GCACTGGTTT TGGTGCATCT ATGTTGATCA AGCAGTTACT TGAAAAGGGT
201 TATGCTGTTA ATACTACCGT TAGAGACCCA GATAGCCCTA AGAAAATATC
251 TCACCTAGTG GCAC TGCAAA GTTGGGGGA ACTGAATCTA TTTAGAGCAG
301 ACTTAACAGT TGAAGAAGAT TTTGATGCTC CTATAGCAGG ATGTGAACCT
351 GTTTTCAAC TTGCTACACC TGTGAACCTT GCTTCTCAAG ATCCTGAGAA
401 TGACATGATA AAGCCAGCAA TCAAAGGTGT GTTGAATGTG TTGAAAGCAA
451 TTGCAAGAGC AAAAGAAGTT AAAAGAGTTA TCTTAACATC TTCGGCAGCC
501 GCGGTGACTA TAAATGAAC TAAAGGGACA GGTCACTGTTA TGGATGAAAC
551 CAACTGGTCT GATGTTGAAT TTCTCAACAC TGCAAAACCA CCCACTTGGG
601 GTTATCCTGC CTCAAAAATG CTAGCTGAAA AGGCTGCATG GAAATTTGCT
651 GAAGAAAATG ACATTGATCT AATCACTGTG ATACCTAGTT TAACAACCTGG
701 TCCTTCTCTC ACACCAAGATA TCCCACATCTAG TGTTGGCTTG GCAATGTCTC
751 TAATAACAGG CAATGATTTC CTCATAAAATG CTTTGAAAGG AATGCAGTTT
801 CTGTCGGGTT CGTTATCCAT CACTCATGTT GAGGATATTT GCCGAGCTCA
851 TATATTTCTT GCAGAGAAAG AATCAGCTTC TGTTAGATAC ATTTGCTGTG
901 CTCACAATAC TAGTGTCCC GAGCTGCAA AGTTTCTCAA CAAACGATAT
951 CCTCAGTATA AAGTTCCAAC TGAATTGAT GATTGCCCA GCAAGGCAA
1001 GTTGATAATC TCTTCTGAAA AGCTTATCAA AGAAGGGTTC AGTTTCAAGC
1051 ATGGTATTGC CGAAACTTTC GACCAGACTG TCGAGTATTT TAAGACTAAG
1101 GGGGCACTGA AGAATTAGAT TTGATATTT CTAATTCAAT AGCAAACTCT
1151 AAGCTTGTGTTA TGTGTTGTG AAGTTCAGAG TGAAATATCA AATGAATAAG
1201 TGGAGAGAGC ACAATAAGAG GAGAGCACAA TAATTTGGA AAAAAAAA
1251 AAAAAAAA AAAAAAAAGT ACTCTGCGTT GTTACCACTG CTTAATCACT
1301 AGTGAATTG

FIGURE 18

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1 MASIKQIGNK KACVIGGTGF VASMLIKQLL EKGYAVNTTV RDPDSPKKIS
51 HLVALQSLGE LNLFRADLTW EEDFDAPIAG CELVFQLATP VNFAASQDPEN
101 DMIKPAIKGV LNVLKAIARA KEVKRVILTS SAAAVTINEL KGTGHVMDT
151 NWSDVEFLNT AKPPTWGYPA SKMLAEKAAW KFAEENDIDL ITVIPSLLTG
201 PSLTPDIPSS VGLAMSLITG NDFLINALKG MQFLSGSLSI THVEDICRAH
251 IFLAEKESAS GRYICCAHNT SVPELAFLN KRYPQYKVPT EFDDCP SKAK
301 LIISSEKLIK EGFSFKHGIA ETFDQTVEYF KTKGALKN

FIGURE 19

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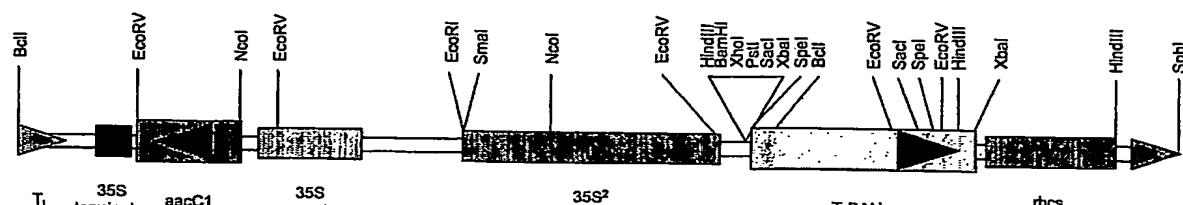
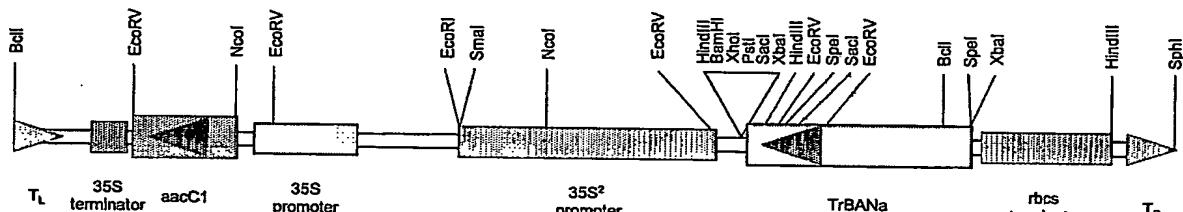
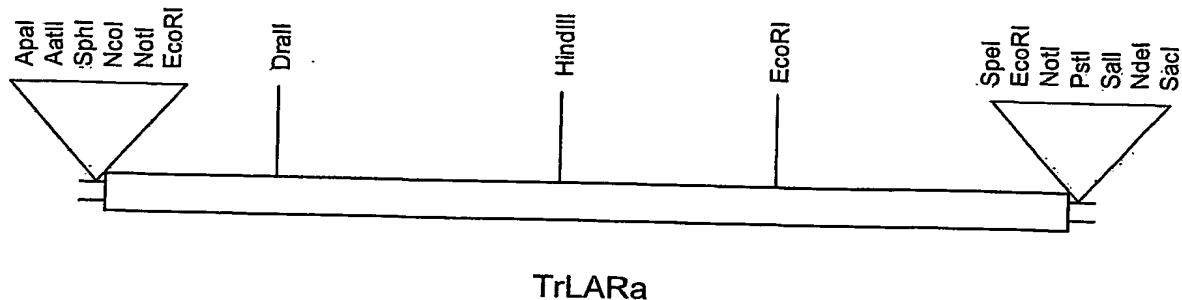
pPZP221:35S²TrBANa sensepPZP221:35S²TrBANa anti

FIGURE 20

22/40**FIGURE 21**

23/40

1 GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GATACCAACA
51 TTGTCACAAT TAACTCTAAA AGCAAAGCAA TGGCACCAGC AGCAACATCA
101 TCACCAACCA CTCCCTACTAC TACCAAGGGT CGTGTCTAA TTGTTGGAGG
151 AACAGGTTTC ATTGGAAAAT TTGTAACTGA GGCAAGTCTT TCCACAAACAC
201 ACCCAACCTA CTTGTTGGTT CGGCCAGGAC CTCTTCTCTC TTCTAAGGCT
251 GCCACTATTA AGGCATTCCA AGAGAAAGGT GCCATTGTCA TTTATGGTCG
301 GGTAAATAAT AAGGAGTTCA TGGAGATGAT TTTGAAAAAG TATGAGATAA
351 ATGTAGTCAT TTCTGCAATA GGAGGCTCTG ATGGCTTGCT GGAACAGCTT
401 ACTTTGGTGG AGGCCATGAA ATCTATTAAC ACCATTAAGA GGTTTTGCC
451 TTCGGAATTG GGTACGATG TGGACAGAGC AAATCCTGTG GAACCTGGCC
501 TAACAATGTA CAAACAGAAA CGTTGGTTA GACGTGTGAT CGAAGAATCT
551 GGTATACCAT ACACCTACAT CTGTTGCAAT TCGATCGCAT CTTGGCCGTA
601 CTATGACAAT TGTCACTCCAT CACAGCTTCC TCCACCGTTG GATCAATTAC
651 ATATTTATGG TCATGGCGAT GTCAAAGCTT ACTTTGTTGA TGGCTATGAT
701 ATTGGGAAAT TCACAATGAA GGTCAATTGAT GATGAAAGAA CAATCAACAA
751 AAATGTTCAT TTTGACCTT CTAACAATTG TTATAGCATG AATGAGCTTG
801 CTTCTTTGTG GGAAAACAAA ATTGCACGAA AAATTCCCTAG AGTGATCGTC
851 TCTGAAGACG ATCTTCTAGC AATAGCCGCA GAAAATTGCA TACCGGAAAG
901 TGTCGTGGCA CCAATCACTC ATGATATATT CATCAATGGA TGTCAAGTTA
951 ACTTCAAGAT AGATGGAATT CATGATGTTG AAATTGGCAC TCTATATCCT
1001 GGTGAATCGG TAAGAAGTTT GGAGGAATGC TATGAGAAAT TTGTTGTCAT
1051 GGCAGGCTGAC AAGATTCTATA AAGAAGAAAC TGGAGTTACC GCAGGTGGGG
1101 GCGGCACAAAC GGCTATGGTA GAGCCGGTGC CAATCACAGC TTCCTGTTGA
1151 AAAGGTTCAC CTGAGGTGGA TATTCTTTG AGTCATAAGA CATGTTGATT
1201 GTTGATGTTG TTTCAAGAA TGTTCTCATCA TTTCATGTGT TTTATTAATC
1251 CTAAGTACAA ATAATTGCTG TCTACGTACG TTCTTAGTTG CAAAAATTCT
1301 TGTTATTCTC TATTGAGGTA AAAGTCTTCA TGTTTACAAA AAAAAAAA
1351 AAAAAAAA AAAAAAAAGT ACTCTGCGTT GTTACCACTG CTTAATCACT
1401 AGTGAATTC

FIGURE 22

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1 MAPAATSSPT TPTTKGRVL IVGGTFIGK FVTEASLSTT HPTYLLVRPG
51 PLLSSKAATI KAFQEKGAIIV IYGRVNNKEF MEMILKKYEI NVVISAIGGS
101 DGLLEQLTLV EAMKSINTIK RFLPSEFGHD VDRANPVEPG LTMYKQKRLV
151 RRVIEESGIP YTYICCNSIA SWPYYDNCHP SQLPPPLDQL HIYGHGDVKA
201 YFVDGYDIGK FTMKVIDDER TINKNVHFRP SNNCYSMNEL ASLWENKiar
251 KIPRVIVSED DLLAIAAENC IPESVVAPIT HDIFINGCQV NFKIDGIHDV
301 EIGTLYPGES VRSLEECYEK FVVMAADKIH KEETGVTAGG GGTTAMVEPV
351 PITASC

FIGURE 23

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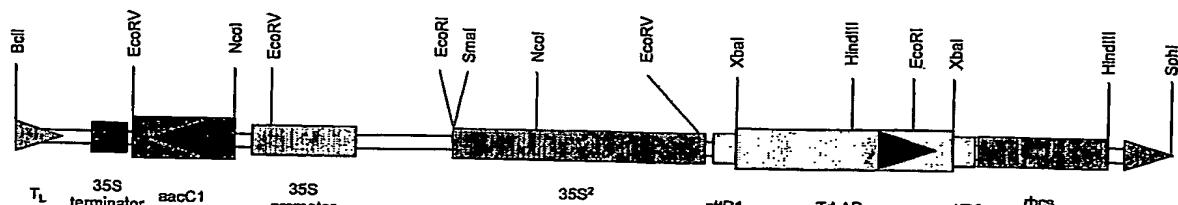
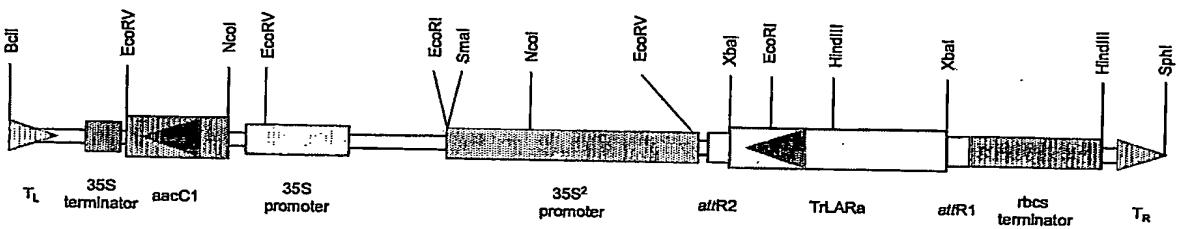
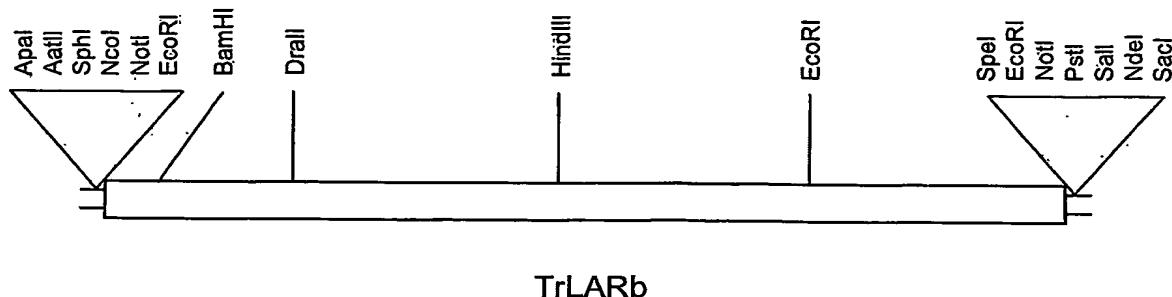
pPZP221:35S²TrLARa sensepPZP221:35S²TrLARa anti

FIGURE 24

26/40**FIGURE 25**

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1 GAATTCTGATT AAGCAGTGTT AACAAACGCAG AGTACGCGGG AGGATCCTTC
51 CATTTCGCAT ACCAACATTG TCACAATTAA CTCTAAAAGC AAAGCAATGG
101 CACCAGCAGC AACATCATCA CCAACCACTC CTACTACTAC CAAGGGTCGT
151 GTCCTAATTG TTGGAGGAAC AGGTTTCATT GGAAAATTG TAACTGAGGC
201 AAGTCTTCC ACAACACACC CAACCTACTT GTTGGTTCGG CCAGGACCTC
251 TTCTCTCTTC TAAGGCTGCC ACTATTAAGG CATTCCAAGA GAAAGGTGCC
301 ATTGTCAATT ATGGTCGGGT AAATAATAAG GAGTTCATGG AGATGATTT
351 GAAAAAGTAT GAGATAAAATG TAGTCATTC TGCAATAGGA GGCTCTGATG
401 GCTTGCTGGA ACAGCTTACT TTGGTGGAGG CCATGAAATC TATTAACACC
451 ATTAAGAGGT TTTTGCCTTC AGAATTTGGT CACGATGTGG ACAGAGCAAA
501 TCCTGTGGAA CCTGGCCTAA CAATGTACAA ACAGAAACGT TTGGTTAGAC
551 GTGTGATCGA AGAATCTGGT GTACCATACA CCTACATCTG TTGCAATTG
601 ATCGCATCCT GGCGTACTA TGACAATTGT CATCCATCAC AGCTTCCTCC
651 ACCGTTGGAT CAATTACATA TTTATGGTCA TGGCGATGTC AAAGCTTACT
701 TTGTTGATGG CTATGATATT GGGAAATTCA CAATGAAGGT CATTGATGAT
751 GAAAGAACAA TCAACAAAAA TGTCATTT CGACCTTCTA ACAATTGTTA
801 TAGCATGAAT GAGCTTGCTT CTTTGTGGGA AAACAAAATT GCACGAAAAA
851 TTCCTAGAGT GATCGTCTCT GAAGACGATC TTCTAGCAAT AGCCGCAGAA
901 AACTGCATAC CGGAAAGTGT TGTGGCATCA ATCACTCATG ATATATTCAT
951 CAATGGATGT CAAGTTAACT TCAAGGTAGA TGGAATTCAT GATGTTGAAA
1001 TTGGCACTCT ATATCCTGGT GAATCGGTA GAAGTTGGG GGAATGCTAT
1051 GAGAAATTG TTGTCATGGC GGCTGACAAG ATTCAAAAG AAGAAACTGG
1101 AGTTACCGCA GGTGGGGCG GCACAAACGGC TATGGTAGAG CCGGTGCCAA
1151 TCACAGCTTC CTGTTGAAAA GGTCACCTG AGGTGGATAT TCTTTGAGT
1201 CATAAGACAT GTTGATTGTT GATGTTGTT TCAAGAATGT TTCATCATT
1251 CATGTGTTT ATTAATCCTA AGTACAAATA ATTGCTGTCT ACGTACGTTC
1301 TTAGTTGCGA AAATTCTTGT TATTCTCTAT TGGGGTAAAA GTCTTCATGT
1351 TTATTGTAGT TGTGTTGGTT TTTCATATAT GCTATTTGCA ATAATGATTT
1401 TTGTGAAGCA CTTGTGGTGT ATTTACTTAC TACTGAAAAT AATGGTTACA
1451 CAAAATATAT AAAAAAATAA AAATAAGCAA AAAAAAAA AAAAAAAA
1501 AAAAAAAA GTACTCTGCG TTGTTACAC TGCTTAATCA CTAGTGAATT
1551 C

FIGURE 26

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1 MAPAATSSPT TPTTKGRVL IVGGTGFIGK FVTEASLSTT HPTYLLVRPG
51 PLLSSKAATTI KAFQEKGAIIV IYGRVNNKEF MEMILKKYEI NVVISAIGGS
101 DGLLEQLTLV EAMKSINTIK RFLPSEFGHD VDRANPVEPG LTMYKQKRLV
151 RRVIEESGVP YTYICCNSIA SWPYYDNCHP SQLPPPLDQL HIYGHGDVKA
201 YFVDGYDIGK FTMKVIDDER TINKNVHFRP SNNCYSMNEL ASLWENKIA
251 KIPRVIVSED DLLAIAAAENC IPESVVASIT HDIFINGCQV NFKVDGIHDV
301 EIGTLYPGES VRSLEECYEK FVVMAADKIH KEETGVTAGG GGTTAMVEPV
351 PITASC

FIGURE 27

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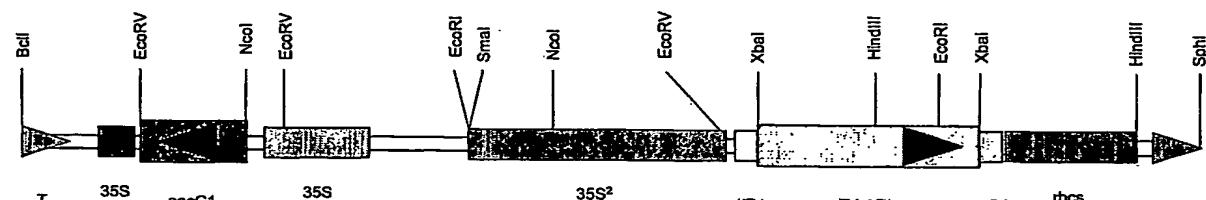
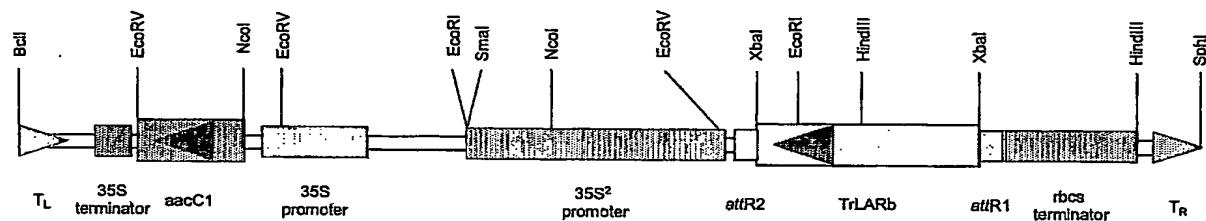
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FIGURE 28

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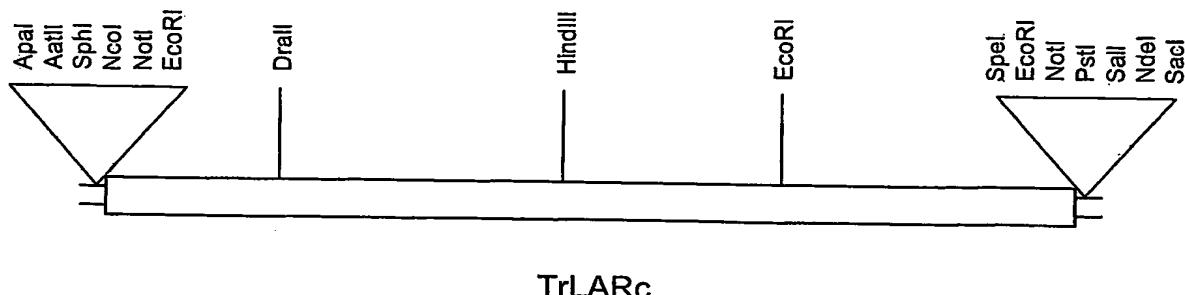


FIGURE 29

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1 GAATTCGATT AAGCAGTGGT AACAAACGCCAG AGTACGCGGG GATACCAACA
51 TTGTCACAAT TAACTCTAAA AGTAAAGCAA TGGCACCAGC AGCAACATCA
101 TCACCCAACCA CTCCCACCTAC TACCAAGGGT CGTGTCTAA TTGTTGGAGG
151 AACAGGTTTC ATTGGAAAAT TTGTAACTGA GGCAAGTCTT TCCACAACAC
201 ACCCAACCTA CTTGTTGGTT CGGCCAGGAC CTCTTCTCTC TTCTAAGGCT
251 GCCACTATTA AGGCATTCCA AGAGAAAGGT GCCATTGTCA TTTATGGTCG
301 GGTAAATAAT AAGGAGTTCA TGGAGATGAT TTTGAAAAAG TATGAGATAA
351 ATGTAGTCAT TTCTGCAATA GGAGGCTCTG ATGGCTTGCT GGAACAGCTT
401 ACTTTGGTGG AGGCCATGAA ATCTATTAAC ACCATTAAGA GGTTTTGCC
451 TTCGGAATTT GGTCACGATG TGGACAGAGC AGATCCTGTG GAACCTGGCC
501 TAACAATGTA CAAACAGAAA CGTTTGGTTA GACGTGTGAT CGAAGAATCT
551 GGTATACCAT ACACCTACAT CTGTTGCAAT TCGATCGCAT CTTGGCCGTA
601 CTATGACAAT TGTCAATCCAT CACAGCTTCC TCCACCGTTG GATCAATTAC
651 ATATTTATGG TCATGGCGAT GTCAAAGCTT ACTTTGTTGA TGGCTATGAT
701 ATTGGGAAAT TCACAATGAA GGTCAATTGAT GATGAAAGAA CAATCAACAA
751 AAATGTTCAT TTTGACCTT CTAACAATTG TTATAGCATG AATGAGCTTG
801 CTTCTTTGTG GGAAAACAAA ATTGCACGAA AAATTCCCTAG AGTGATCGTC
851 TCTGAAGACG ATCTTCTAGC AATAGCCGCA GAAAATTGCA TACCGGAAAG
901 TGTCAAGTGGCA CCAATCACTC ATGATATATT CATCAATGGA TGTCAAGTTA
951 ACTTCAAGAT AGATGGAATT CATGATGTTG AAATTGGCAC TCTATATCCT
1001 GGTGAATCGG TAAGAAGTTT GGAGGAATGC TATGAGAAAT TTGTTGTCAT
1051 GGCGGCTGAC AAGATTCTA AAGAAGAAAC TGGAGTTACC GCAGGTGGGG
1101 GCGGCACAAC GGCTATGGTA GAGCCGGTGC CAATCACAGC TTCCCTGTTGA
1151 AAAGGTTCAC CTGAGGTGGA TATTCTTTG AGTCATAAGA CATGTTGATT
1201 GTTGATGTTG TTTTCAAGAA TGTTTCATCA TTTCATGTGT TTTATTAATC
1251 CTAAGTACAA ATAATTGCTG TCTACGTACG TTCTTAGTTG CAAAAATTCT
1301 TGTTATTCTC TATCAAAAAA AAAAAAAA AAAAAAAA AAAGTACTCT
1351 GCGTTGTTAC CACTGCTTAA TCACTAGTGA ATTC

FIGURE 30

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1 MAPAATSSPT TPTTKGRVL IVGGTGFIGK FVTEASLSTT HPTYLLVRPG
51 PLLSSKAATI KAFQEKGAIY IYGRVNNKEF MEMILKKYEI NVVISAIGGS
101 DGLLEQLTLV EAMKSINTIK RFLPSEFGHD VDRADPVEPG LTMYKQKRLV
151 RRVIEESGIP YTYICCNSIA SWPYYDNCHP SQLPPPLDQL HIYGHGDVKA
201 YFVDGYDIGK FTMKVIDDER TINKNVHFRP SNNCYSMNEL ASLWENKIA
251 KIPRVIVSED DLLAIAAENC IPESVVAPIT HDIFINGCQV NFKIDGIHDV
301 EIGTLYPGES VRSLEECYEK FVVMAADKIH KEETGVTAGG GGTTAMVEPV
351 PITASC

FIGURE 31

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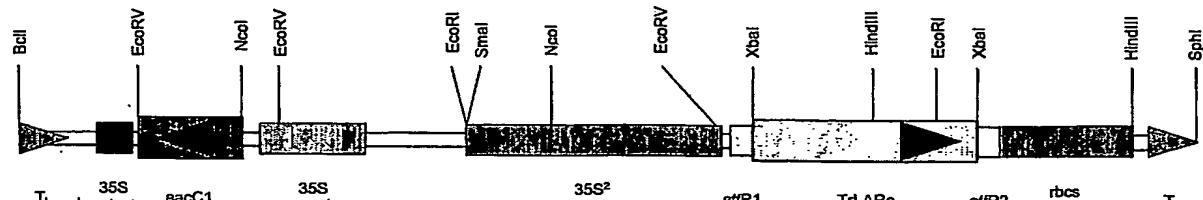
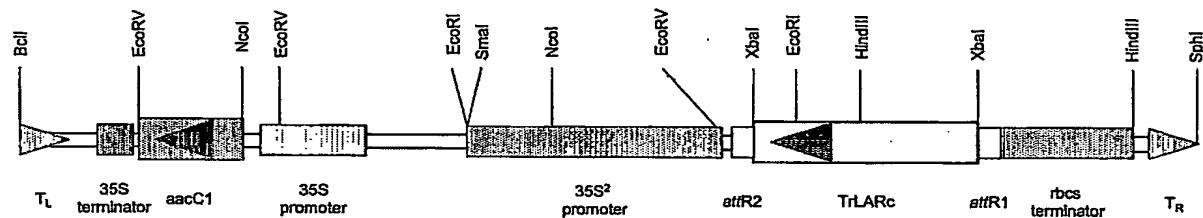
pPZP221:35S²TrLARc sensepPZP221:35S²TrLARc anti

FIGURE 32

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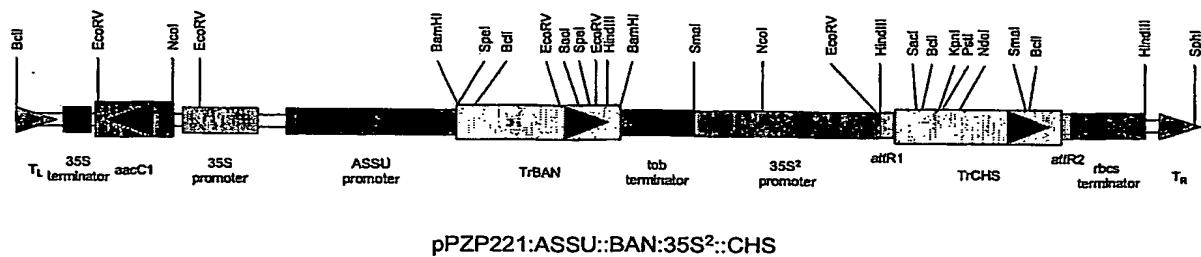


FIGURE 33

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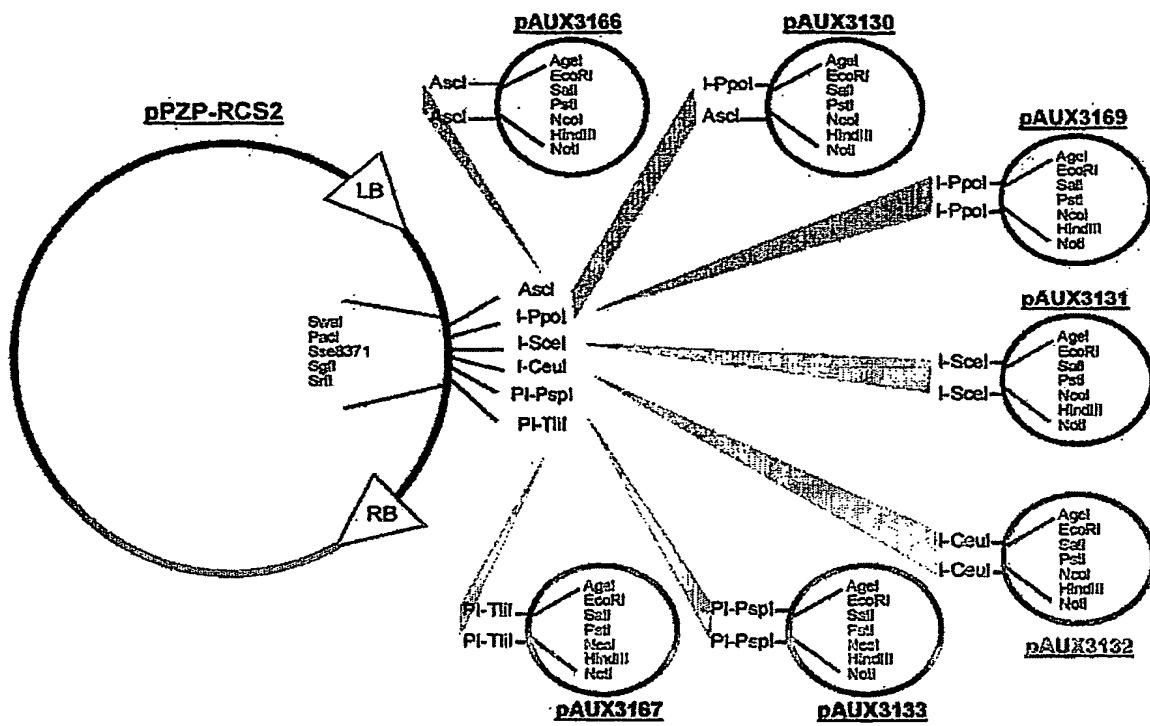


FIGURE 34

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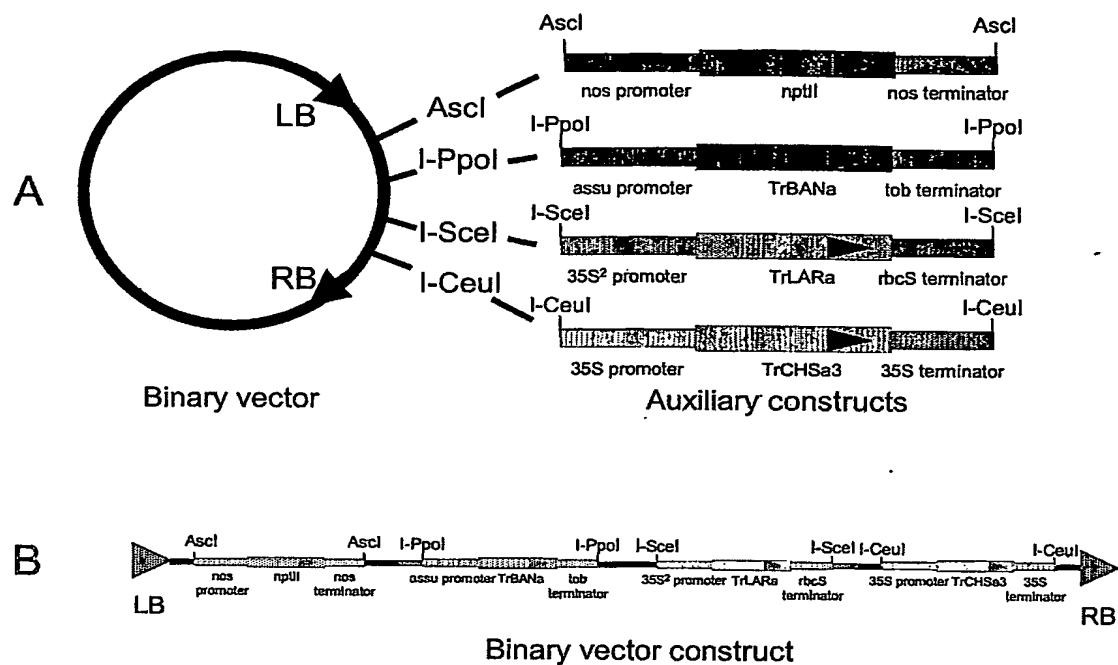


FIGURE 35

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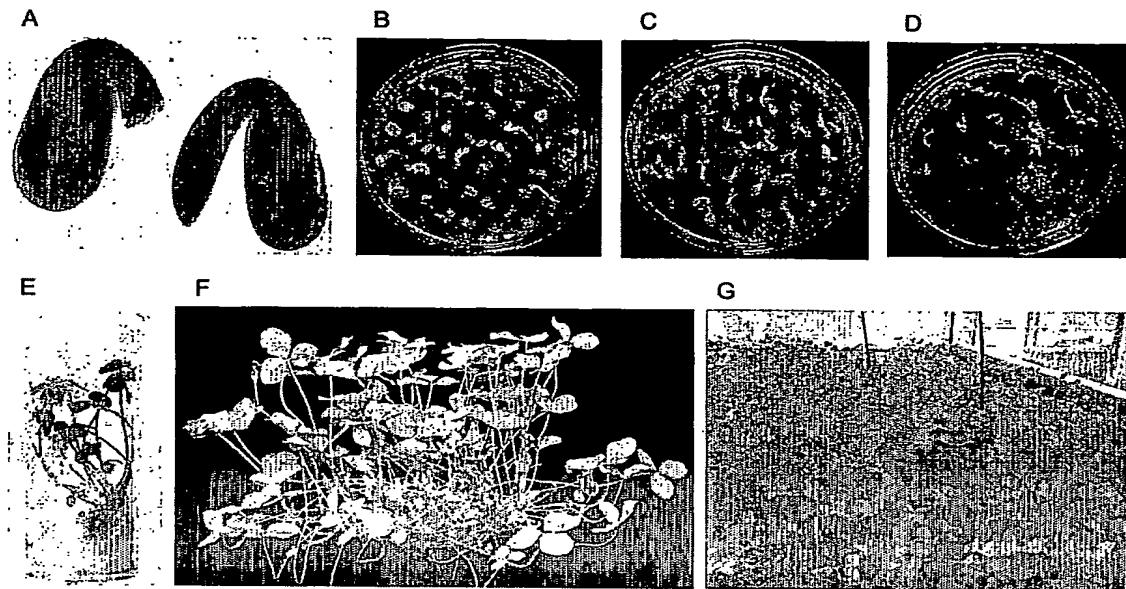


FIGURE 36

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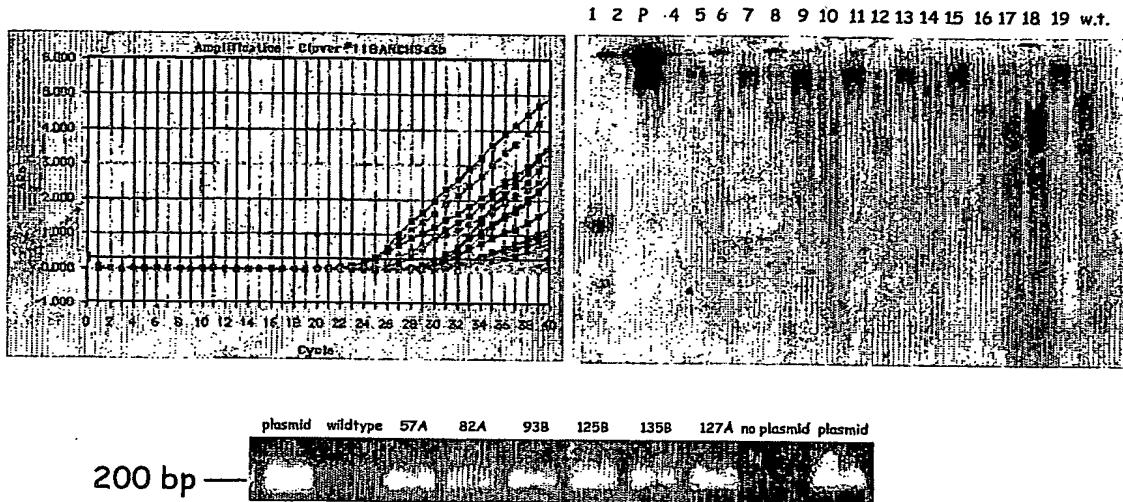
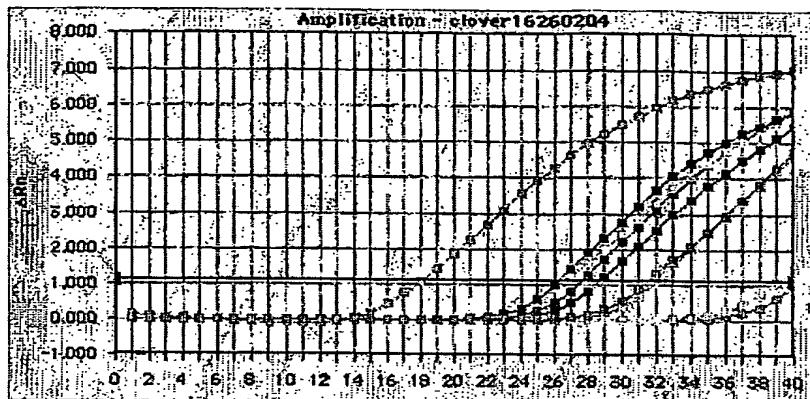
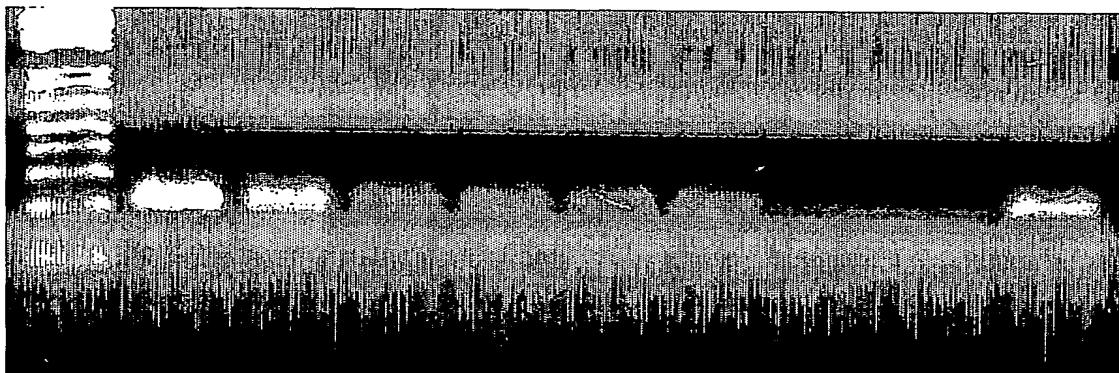
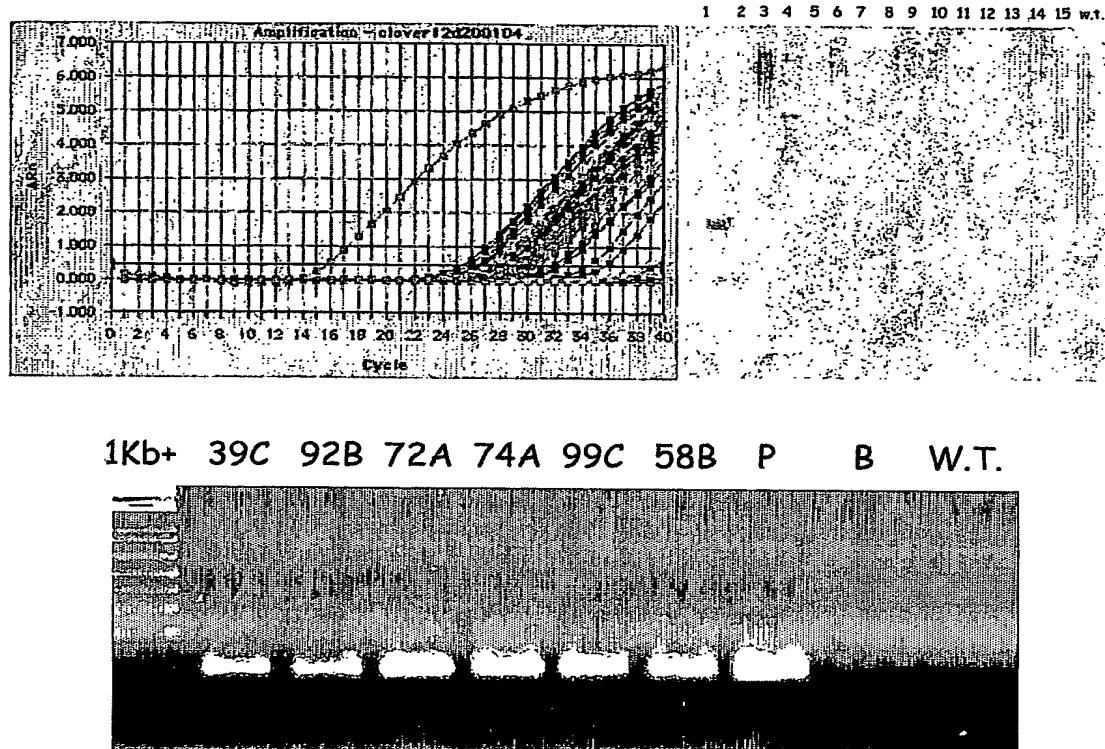


FIGURE 37

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1Kb+ 3A 22A 6B 24A 34A 29E Blank W.T. P

**FIGURE 38**

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